REMARKS

Reconsideration of the present application is respectfully requested. Claims 1-15, 23, 24, 32, 33, 41-45, 49-59, 65-71 and 73-75 are pending. Claims 11, 56, 65, 66, and 73, have been amended. Support for the amendments is found in the original claims. Claim 15 has been cancelled and rewritten as new claim 76. Support for the new claim is found in the claims as originally filed. Claims 74 and 75 have been cancelled. Figures 1-4 have been cancelled. The specification has been amended to remove references to the Figures.

Two original inventors have been deleted under 37 CFR §1.48(b) who are not inventors of the now claimed subject matter. A petition is attached to this paper identifying each inventor and acknowledging that their invention is no longer being claimed.

The marked up version of the claim and specification amendments is found on a separate sheet attached to this amendment and titled "Version with Markings to Show Changes." It is respectfully requested that the amendments be entered.

Rejections under 35 U.S.C. §112

Rejections under 35 USC §112, second paragraph:

Claims 1-13, 15, 24, 33, 41-44, 50-52, 71 and 73 are rejected under §112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

The Examiner states: "[The] [C]laims ...are indefinite for the language 'hybridizes under stringent conditions' since neither the art nor the specification as filed provide the conditions which define stringent conditions...."

"Stringent conditions" are thoroughly defined and discussed in the specification as filed beginning on page 10, line 23, through page 12, line 13 with particularly relevant detail on page 10, line 23, and page 11, lines 3 and 27.

The Examiner states: "Claim 15 is indefinite since the ending is missing. It appears there should be a step (g) which was inadvertently omitted."

The Examiner is thanked for bringing this to Applicant's attention. Claim 15 has been cancelled and rewritten as new claim 76 which adds step (g) which was inadvertently omitted.

The Examiner states: "Claims 41, 43, and 73 lack antecedent basis since they depend on canceled claims."

Claims 41 and 43 were amended via preliminary amendment filed November 30, 1999 to depend from claim 32. Claim 73 has been amended in the current paper to properly depend from claim 71.

The Examiner states: "In claims 56, 65, and 66 'said nucleotide sequence' lacks antecedent basis."

Claims 56, 65, and 66 have been amended to recite "...at least one *nucleotide* sequence..." to provide proper antecedent basis.

Rejections under 35 USC §112, first paragraph:

Claims 1-15, 23-24, 32, 33, 41-45, 49-59, 65-71 and 73-75 are rejected under 35 USC §112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The Examiner states: "The claims are drawn to nucleic acid and protein sequences encoding any plant GDP-mannose pyrophosphorylase, ... The specification as filed teaches the sequence of the maize GDP-mannose pyrophosphorylase gene in SEQ ID NO:1 and the sequence of the maize GDP-mannose pyrophosphorylase protein in SEQ ID NO:2. ...Neither the art nor the specification as filed teach the sequences of other plant GDP-mannose pyrophosphorylase sequences at the time the invention was made...."

The Federal Register (vol.66, no.4, Jan. 5, 2001, page1106, column 3, third paragraph) recites: "For each claim drawn to a genus: The written description requirement for a claimed genus may be satisfied through sufficient description of a representative number of species by actual reduction to practice....reduction to drawings....*or by disclosure of relevant, identifying characteristics, i.e., structure or other physical and/or chemical properties, by functional characteristic coupled with a known or disclosed correlation between function and structure, or by a combination of such identifying characteristics sufficient to show the applicant was in possession of the claimed genus.*"

The application discloses structure via a full-length cDNA sequence (SEQ ID NO:1) and the corresponding protein sequence (SEQ ID NO:2) of a plant GDP-mannose pyrophosphorylase represented by maize. The application discloses the function correlated with these structures on page 4, lines 15-17: "The formation of the substrate GDP-mannose, from mannose-1-phosphate and GTP, is catalyzed by the enzyme GDP- mannose pyrophosphorylase." And again on page 7, lines 13-15: "Thus, for purposes of the present invention, a functionally equivalent variant of GDP- mannose pyrophosphorylase will catalyze the formation of GDP-mannose, from mannose-1-phosphate and GTP."

Physical and chemical properties associated with the claimed sequences are defined by hybridization conditions to the disclosed sequence on pages 10, line 23, through page 12, line 13; and by percent identity to the disclosed sequence described on page12, lines 14-29.

The test for sufficiency of support in a parent application is whether the disclosure of the application relied upon "*reasonably* conveys to the artisan that the inventor had possession at that time of the later claimed subject matter." (MPEP 2163.02)

By disclosing the foregoing identifying characteristics, it is believed that one of skill in the art would reasonably conclude that the applicant was in possession of the claimed invention.

The Examiner continues: "...it would not have been clear to one of skill in the art at the time the invention was made what the metes and bounds of the genus of possible sequences encompassed by the invention as broadly claimed would have been ... an assumed related functionality between major components of biosynthetic pathways common to all plants would still not lead one of skill in the art at the time the invention was made to identify a clear set of structural parameters for which all such GDP-mannose pyrophosphorylase genes would have so that there would have been expectation to based on structure whether a sequence will function as a plant GDP-mannose pyrophosphorylase."

The metes and bounds of the presently claimed invention are described both functionally and structurally. First by reference to the function of the sequence: the claimed sequences must function as a plant GDP-mannose pyrophosphorylase as described above. Next, structurally by "having at least 90% identity" to a nucleotide identified functionally as a plant GDP-mannose pyrophosphorylase, or to a nucleotide having the nucleotide sequence of SEQ ID NO:1, or to a nucleotide encoding the amino acid sequence of SEQ ID NO: 2. Finally, the claimed invention is described physically/chemically as "a nucleotide sequence that hybridizes ... under stringent conditions" to a nucleotide identified functionally as a plant GDP-mannose pyrophosphorylase, or to a nucleotide having the nucleotide sequence of SEQ ID NO:1, or to a nucleotide encoding the amino acid sequence of SEQ ID NO: 2. Based on the information given in the specification as cited herein, one of skill in the art could easily visualize a polynucleotide within the metes and bounds of the present claims.

The Examiner cites Kellar et al. as one of skill in the art. It is instructive to note that Kellar et al use the same technique for isolating potato GDP-mannose pyrophosphorylase (abbreviated to GMPase) as disclosed in the present specification (see Example 1, page 18) by isolating clones from a plant tissue library and comparing homology to the *Saccharomyces cerevisiae* GDP-mannose pyrophosphorylase (see Kellar et al., page 132, first column, first paragraph under "Results").

The Examiner continues: "For the claims which broadly read on any sequence which hybridizes to at least a 20 base portion of SEQ ID NO:1, and any variant of the protein of SEQ ID NO:2, the genus would have an expectation in the art to read on multiple sequences which have no related function to a plant GDP- mannose pyrophosphorylase."

The MPEP states in section 2164.08(b): "The presence of inoperative embodiments within the scope of the claim does not necessarily render a claim nonenabled. The standard is whether a skilled person could determine which embodiments that were conceived, but not yet made, would be inoperative or operative with expenditure of no more effort than is normally required in the art."

The Examiner concludes: "In view of the breadth of genus of possible sequences, one skilled in the art would not have been in possession of the scope of the possible sequences claimed,.... Neither the art nor the specification as filed teach a representative number of species for the breadth of the genus of possible sequences claimed."

It is not necessary to teach a representative number of species if "one of skill in the art would recognize that the application was in possession of the necessary common attributes or features of the elements possessed by the members of the genus in view of the species disclosed." (Fed. Reg. vol. 66, no.4 Jan. 5, 2001, page 1106, column 3, third paragraph.)

The application has described common attributes in term of function and structure as discussed above such that the skilled artisan could readily visualize that the applicant was in possession of the invention claimed.

The Rules repeatedly state that: "The examiner has the initial burden, after a thorough reading and evaluation of the content of the application. of present evidence or reasons why a person skilled in the art would not recognize that the written description of the invention provides support for the claims." (Fed. Reg., Vol. 66, No.4 Jan. 5, 2001, page 1105, column 2, paragraph II (a)).

The Examiner has not presented evidence or reasoning to show that the genus claimed in the present invention has such substantial variation that the structural, functional, and physical parameters described in the specification and cited herein, do not enable the present invention.

Claims 1-15, 23-24, 32-33, 41-45, 49-55, 65-71 and 73-75 are rejected under 35 U.S.C. §112, first paragraph, because the specification does not reasonably provide enablement for the scope of possible nucleic acid sequences or protein sequences claimed nor use thereof in plant cells or plants.

Claims 15, 74, and 75 have been cancelled. Claim 15 has been re-written as new claim 76.

The Examiner states: "Applicant has provided little or no guidance beyond the mere presentation of sequence data to enable one of ordinary skill in the art to determine, without undue experimentation, the positions in the protein which are tolerant to change (e.g. such as by amino acid substitutions or deletions), and the nature and extent of changes that can be made in these positions."

It is respectfully requested that the Examiner make explicit which claims the statement refers to. Variants and/or amino acid substitutions of the coding region are not claimed in the present invention.

The Examiner states: "Although the specification outlines art-recognized procedures for producing and screening for active muteins, this is not adequate

guidance as to the nature of active derivatives that may be constructed, but is merely an invitation to the artisan to use the current invention as a starting point for further experimentation."

It is respectfully requested that the Examiner make explicit which claims the statement refers to. Muteins and/or derivatives of the coding region are not claimed in the present invention.

The Examiner states: "The art recognizes that function cannot be predicted from structure alone.... Due to the large quantity of experimentation necessary to generate the infinite number of derivatives recited in the claims and possibly screen same for activity, the lack of direction/guidance presented in the specification regarding which structural features are required in order to provide activity, the absence of working examples directed to same, the complex nature of the invention, the state of the prior art which establishes the unpredictability of the effects of mutation on protein structure and function, and the breadth of the claims which fail to recited any structural or functional limitations, undue experimentation would be required of the skilled artisan to make an/or use the claimed invention in it's full scope."

The Examiner is requested to explicitly state which claims the above statement refers to. The present invention does not claim derivatives or mutations of the coding region.

Present claim one recites: "1. An isolated nucleotide sequence selected from the group consisting of: a) a nucleotide sequence encoding a plant GDP-mannose pyrophosphorylase; b) a nucleotide sequence encoding the amino acid sequence of SEQ ID NO:2; c) a nucleotide sequence set forth in SEQ ID NO:1; d) a nucleotide sequence comprising at least 20 contiguous nucleotides of SEQ ID NO:1; e) a nucleotide sequence having at least 90% identity to a nucleotide sequence of a), b), c) or d); f) a nucleotide sequence that hybridizes to a nucleotide sequence of a), b), c), d) or e) under stringent conditions; and g) a

nucleotide sequence encoding an antisense RNA of a nucleotide sequence of a), b), c), d), e) or f) ;and fragments and variants thereof."

It is respectfully submitted that one skilled in the art would reasonably expect that those nucleic acid molecules that hybridize under stringent conditions and have at least 90% identity to SEQ ID NO:1, and possess GDP-mannose pyrophosphorylase activity would be encompassed by the present claims. The skilled artisan would recognize that the limitations of Claim 1 are such that a majority of nucleic acid sequences encompassed by the claim would be expected to be functional. The functional and structural limitations of present Claim 1 preclude undue experimentation.

The Examiner states: "The assertion that the disclosed sequences have biological activities similar to any other possible isolated sequence having homology, or which hybridizes to the disclosed sequences cannot be accepted in the absence of supporting evidence, because the *relevant literature* reports example of polypeptide families wherein individual members have distinct, and sometimes even opposite, biological activities."

The Examiner cites Tischer et al., Benjamin et al., Vukicevic et al., Pilbeam et al., and Kopchick et al. as relevant literature.

It is pointed out that of the above-cited references, none relate to plants. All the cited references concern human or other mammalian systems.

The Examiner states: "Generally, the art acknowledges that function cannot be predicted based solely on structural similarity to a protein found in the sequence databases." The Examiner cites references that recite a number of pitfalls in blindly accepting an assigned function to a sequence in a database.

The Examiner is reminded that: "There is a strong presumption that an adequate written description of the claimed invention is present in the specification as filed." (Fed. Reg., Vol. 66, No.4 Jan. 5, 2001, page 1105, column 2, paragraph II (a)).

The Examiner's attention is drawn to the attached amino acid sequence homology table. The table contains six plant and two yeast GDP-mannose pyrophosphorylase sequences. It is clear there are a sufficient number of conserved regions to indicate to one of skill in the art searching a database that there could be little doubt as to the function of the maize sequence. Further, as noted by the Examiner, the potato sequence was found to be functional as a transgene in *E coli* (Kellar et al., page 132, column 2, paragraph two) although the sequence homology between the potato enzyme and the yeast enzyme used to identify it was as low as 60.6% (Kellar et al., page 132, column 2, lines 1 and 2).

The Examiner concludes: "Due to the large quantity of experimentation necessary to determine an activity or property of any sequence such that it can be determined how to use the claimed nucleic acids or polynucleotides encoding any plant GDP-mannose pyrophosphorylase, the lack of direction/guidance presented in the specification regarding same, the absence of working examples directed to same, the complex nature of the invention, the state of the prior art establishing that biological activity cannot be predicted based on structural similarity, and the breadth of the claims which fail to recite particular biological activities and also embrace a broad class of structural fragments and variants, undue experimentation would be required of the skilled artisan to make and/or use the claimed invention in it's full scope."

As stated above, one skilled in the art would reasonably expect that those nucleic acid molecules that hybridize under stringent conditions, have at least 90% identity to SEQ ID NO:1, and possess GDP-mannose pyrophosphorylase activity could be used in the presently claimed invention. Methods for determining hybridization conditions and percent identities are well known and routine in the art and have been cited previously. Testing for GDP-mannose

pyrophosphorylase activity is also well known and cited on page 17 of the specification beginning on line 28.

The specification presents ample direction and guidance for using the claimed nucleic acids. Methods for making expression cassettes are given on page 13 line 1 through page 16, line 18; for transforming plants: page 16, line 17, through page 17, line 27; and methods for testing transformed plants or plant cells for expression of GDP-mannose pyrophosphorylase: page 17, line 28, through page 18, line 3.

Also prophetic examples of expression cassette construction, and plant transformation are presented in Examples 1 and 2 (pages 18 and 19 of the specification, respectively). Regarding the Examiner's concern about a lack of working examples, the MPEP states: "Compliance with the enablement requirement of 35 USC §112, first paragraph, does not turn on whether an example is disclosed. An example may be "working" or "prophetic"." (MPEP sec. 2164.02, first paragraph).

Further, the state of the prior art does not state that biological activity *cannot* be predicted by structure, but rather that one of skill in the art must take special consideration when assigning function on the basis of computer homology. "However, there is still no doubt sequence analysis is extremely powerful and that the generation of hypotheses derived by computational methods will be more and more often the first successful step in the design of experiments." (Bork, page 400, column 2, second paragraph).

Finally, regarding the Examiner's concern that: "... the claims [which] fail to recite particular biologcal activities and also embrace a broad class of structural fragments and variants"....the claims recite biological activity in the phrase: "a sequence encoding a plant GDP-mannose pyrophosphorylase". Structural fragments and variants are not claimed in the present invention.

Claims 56-59 are rejected under 35 USC §112, first paragraph as containing subject matter which was not described in the specification in such a way as to enable one skilled in the art to make/use the invention.

Claims 56-59 are drawn to methods for manipulating gum production in a plant of interest via transforming plant cells with at least one nucleic acid sequence encoding an enzyme in a galactomanan biosynthetic pathway.

The Examiner states: "The specification does not teach by way of example that the disclosed maize GMP-mannose pyrophosphorylase [sic] nor any other such possible species of pyrophosphorylase or any possible protein in any plant galactomannan biosythetic [sic] pathway will manipulate gum production in any plant of interest...Neither the specification not the art provide one of skill in the art with the necessarily nexus [sic] to teach how to mainpulate gumproduction in any plant as broadly claimed....Stephanopoulos et al. ... and DeLuca ... are relied upon to teach the unpredictability in the art for predicting phenotypic function based on manipulation of one gene/protein in a biosynthetic pathway."

As noted above, the presence or absence of an example, working or otherwise does not alone preclude enablement.

The Examiner cites De Luca and Stephanopoulos et al to support the contention of "unpredictability in the art for predicting phenotypic function based on manipulation of one gene/protein in a biosynthetic pathway in plants". In fact the references cited by the Examiner offer both examples of success, and teaching for rational design of successful metabolic engineering of plants. De Luca offers no less than eleven examples of success in altering metabolic pathways in plants via transformation with exogenous genes (see De Luca page 225N, paragraph 5; page 226N, paragraph 2; page 227N, paragraphs 2, 3, 4, 5, 7 and 10; and page 228N, paragraphs 2, 3, and 4).

Stephanopoulos et. al. presents extensive principles and methodologies for achieving the desired results in altering metabolic pathways. It is instructive

to note that the teachings of De Luca and Stephanopoulos et al. were published in 1993 and thus were known in the art for six years when the present application was filed, such that one of skill in the art would have every reason to believe that the applicant was in possession of the claimed invention.

"The examiner has the initial burden, after a thorough reading and evaluation of the content of the application, of presenting evidence or reasons why a person skilled in the art would not recognize that the written description of the invention provides support for the claims. There is a strong presumption that an adequate written description of the claimed invention is present in the specification as filed;" (*Federal Register*, Vol.66, No. 4, 01-05-01; p1105, 2nd column, third paragraph).

The Examiner has presented no evidence or cogent technical reasons why a person skilled in the art would not recognize that the specification supports the claimed invention.

The Examiner further states: "...the art teaches that gum production varries [sic] in different species of plants as to the composition of the gum such that the ratio of different components of the gum differs significantly."

The Examiner is asked to provide references for such art. Furthermore, the presently claimed invention does not claim gums of a specific composition.

The Examiner concludes: "In view of the unpredictability in the art as to how increasing or decreasing any particular component of a biosynthetic pathway would effect a particular phenotypic change, one skilled in the art would have to practice "trial and error" experimentation to practice the claimed invention as broadly claimed. Neither the art nor the specification as filed provide guidance as to how increasing or decreasing production of any galactomannan biosynthetic pathway component or any GDP-mannose pyrophosphorylase in any recombinant plant would be useful for manipulation of gum production.

The Examiner's attention is drawn to the specification page 3, lines 2-8 which describes how gums are synthesized in plants. The role of the galactomannan biosynthetic pathway in gum production is well known in the art. Ritter et.al. (cited in the Information Disclosure Statement) characterizes the galactomannan biosynthetic pathway thus: "GDP-mannose is one of the activated sugars that at this time have been extensively examined, and which can be reacted with glycosyl transferases to form oligosaccharides."

Likewise, Betlach et al. (submitted in the Information Disclosure Statement) stresses the importance of GDP-mannose in the production of Xanthan gum, an important industrial gum derived from the bacteria *Xanthomonas campestris*. (Betlach et al. page 3, lines 7-10) As the formation of GDP-mannose is catalyzed by GDP-mannose pyrophosphorylase, it is clear that manipulation of this enzyme would affect gum production whether in plants or in bacteria.

In light of the above remarks, it is submitted that the present specification enables one of ordinary kill in the art to make and use the claimed invention without undue experimentation.

CONCLUSION

On the basis of the above amendments and remarks, reconsideration of the application and it's allowance are respectfully requested.

Respectfully submitted,

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

The paragraph beginning on line 9 of page 4 has been amended as follows:

The present invention discloses compositions and methods for the synthesis of the gum galactomannan in non-legume plants, plant cells and specific tissues, as well as for the increased expression in leguminous plants, plant cells and specific tissues. The methods involve modulation of the levels of enzymes in the galactomannan biosynthetic pathway. The synthesis of the gum galactomannan is catalyzed by the enzymes mannan synthase and galactosyl transferase, from the substrates GDP-mannose and UDP-galactose [(Figure 1)]. The formation of the substrate GDP-mannose, from mannose-1-phosphate and GTP, is catalyzed by the enzyme GDP-mannose pyrophosphorylase.

The paragraph beginning on line 17 of page 5 has been amended as follows:

The present invention is further drawn to compositions and methods for manipulating the levels of enzymes of the galactomannan biosynthetic pathway in plants, plant cells, and specific plant tissues. By enzymes of the galactomannan biosynthetic pathway is meant GDP-mannose pyrophosphorylase, mannan synthase and galactosyl transferase. It is recognized that as the galactomannan pathway is further elucidated, newly discovered galactomannan biosynthetic enzymes are included in the methods of the invention. Compositions are nucleic acids relating to genes encoding enzymes of the galactomannan biosynthetic pathway in plants, preferably to GDP-mannose pyrophosphorylase or GDP-mannose pyrophosphorylase-like

genes. Preferably, the GDP-mannose pyrophosphorylase is native to maize or a leguminous plant. By native to maize or a leguminous plant is meant that the GDP-mannose pyrophosphorylase may be present in a naturally occurring or cultivated species of maize or a leguminous plant. Nucleotide sequences for a maize GDP-mannose pyrophosphorylase gene and the amino acid sequence for the GDP-mannose pyrophosphorylase protein encoded thereby are disclosed, as well as fragments and variants thereof. These sequences are set forth in [Figures 2 (SEQ ID NO:1) and 3 SEQ ID NO:2)] SEQ ID NOS:1 and 2. The maize GDP-mannose pyrophophorylase sequences were disclosed in U.S. provisional application Serial No: 60/096,782, filed 17 August 1998, to which the instant application claims priority and which is incorporated herein by reference. The sequences find use in the construction of expression vectors for subsequent transformation into plants of interest, as probes for the isolation of other GDP-mannose pyrophosphorylase-like genes, as molecular markers, and the like.

The paragraph beginning on line 18 of page 18 has been amended as follows:

A full-length cDNA sequence encoding maize GDP-mannose pyrophosphorylase gene was isolated from the maize genomic project. Maize root and culture cell cDNA libraries were constructed according to the manufacturer's instructions (Gibco-BRL). cDNA clones were partially sequenced from 5 -end. 5 -sequences of cDNA clones were then compared to the Saccharomyces cerevisiae V1G9 GDP-mannose pyrophosphorylase gene (Hashimoto et al., (1997) J. Biol. Chem. 272:16308-16314) with the BlastX subroutine. A clone that showed significant homology to the gene was sequenced completely. The nucleotide sequence and the deduced amino acid sequence are set forth in [Figures 2 (SEQ ID NO:1) and 3 (SEQ ID NO:2)] SEQ ID NOS: 1 and 2, respectively. Gene sequences are cloned into a plasmid vector[, such as that shown in Figure 4,] in the sense orientation so that they are

under the transcriptional control of the ubiquitin promoter. A selectable marker gene may reside on this plasmid or may be introduced as part of a second plasmid. The transformation construct is then available for introduction into maize embryos by bombardment methods as described in Example 2.

In the claims:

11. (Amended) The expression cassette of claim 10, wherein said promoter is selected from the group of promoters consisting of: cim1, cZ19B1, [celA], gama-zein, glob-1 and phaseolin.

56. (Amended) A method for manipulating gum production in a plant of interest, comprising the steps of:

a) transforming plant cells with at least one [nucleic acid] nucleotide sequence encoding an enzyme in a galactomannan biosynthetic pathway or an antisense RNA thereto; wherein said nucleotide sequence is operably linked to a promoter that drives expression in a plant;

b) screening the plant cells transformed in step (a) for stable expression of said enzyme or said antisense RNA to obtain positive cultures;

c) regenerating said positive cultures into a plant; and

d) growing the plant from step (c).

65. (Amended) A recombinant plant cell having stably incorporated into its genome at least one [nucleic acid] nucleotide sequence encoding an enzyme in a galactomannan biosynthetic pathway or an antisense RNA to an enzyme in a galactomannan synthetic pathway; wherein said

nucleotide sequence is operably linked to a promoter that drives expression in a plant.

66. (Amended) A transformed plant having stably incorporated into its genome at least one [nucleic acid] nucleotide sequence encoding an enzyme in a galactomannan biosynthetic pathway or an antisense RNA to an enzyme in a galactomannan synthetic pathway; wherein said nucleotide sequence is operably linked to a heterologous promoter that drives expression in a plant cell.

73. (Amended) Variants of the recombinant protein of claim [72] 71.

New Claim 76 has been added as follows:

76. The method of claim 14, wherein said nucleotide sequence is selected from the group consisting of:

a) a nucleotide sequence encoding a GDP-mannose pyrophosphorylase that is native to maize or a leguminous plant;

b) a nucleotide sequence encoding the amino acid sequence of SEQ ID NO:2;

c) a nucleotide sequence set forth in SEQ ID NO:1;

d) a nucleotide sequence comprising at least 20 contiguous nucleotides of SEQ ID NO:1;

e) a nucleotide sequence having at least 90% identity to a nucleotide sequence of a), b), c) or d);

f) a nucleotide sequence that hybridizes to a nucleotide sequence of a), b), c), d) or e) under stringent conditions; and

g) a nucleotide sequence encoding an antisense RNA of a nucleotide sequence of a), b), c), d), e) or f) ;and fragments and variants thereof.

In the drawings:

Figures 1-4 have been cancelled.

In Inventorship:

Xun Wang and Benjamin A. Bowen have been deleted as inventors.

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Alignment of GDP-mannose pyrophosphorylase from different organisms. Accession numbers are as follows: Arabidopsis1, NP_194786.1; Arabidopsis2, NP_181507.1; Candida, BAA77382.1; Oryza, BAB64272.1; Potato, AAD01737.1; Tobacco, BAB62108.1; Yeast, NP_010228.1.

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                    1                                                  50
Arabidopsis1    (1) --------------------MPKPLVDFGNKPMILHQIEALKGAGVTEVV
Arabidopsis2    (1) MKALILVGGFGTRLRPLTLSFPKPLVDFANKPMILHQIEALKAVGVDEVV
     Candida    (1) MKGLILVGGYGTRLRPLTLTVPKPLVEFGNRPMILHQIEALANAGVTDIV
       Maize    (1) MKALILVGGFGTRLRPLTLSFPKPLVDFANKPMILHQIEALKEVGVTEVV
       Oryza    (1) MKALILVGGFGTRLRPLTLSFPKPLVDFANKPMILHQIEALKEVGVTEVV
      Potato    (1) MKALILVGGFGTRLRPLTLSVPKPLVEFANKPMILHQIEALKAVGVTEVV
     Tobacco    (1) MKALILVGGFGTRLRPLTLSVPKPLVEFANKPMILHQIEALKAVGVTEVV
       Yeast    (1) MKGLILVGGYGTRLRPLTLTVPKPLVEFGNRPMILHQIEALANAGVTDIV
   Consensus    (1) MKALILVGGFGTRLRPLTLSVPKPLVDFANKPMILHQIEALKAVGVTEVV
                   51                                                 100
Arabidopsis1   (31) LAINHQQPEVMLNFVKEYEKKLEIKITFSQETEPLGTAGPLALARDKLVD
Arabidopsis2   (51) LAINYQ-PEVMLNFLKDFETKLEIKITCSQETEPLGTAGPLALARDKLLD
     Candida   (51) LAVNCR-PEVMVETLQKYEKEYGVSITFSVETEPLGTAGPLKLAEKVLKK
       Maize   (51) LAINYR-PEVMINFLKDFEDKLGITITCSQETEPLGTAGPLALARDKLAD
       Oryza   (51) LAINYR-PEVMLNFLKDFEDKLGITITCSQETEPLGTAGPLALARDKLVD
      Potato   (51) LAINYQ-PEVMLNFLKEFEASLGIKITCSQETEPLGTAGPLALARDKLID
     Tobacco   (51) LAINYQ-PEEMLNFLKEFEANLGIKITCSQETEPLGTAGPLALARDKLID
       Yeast   (51) LAVNYR-PEVMVETLKKYEKEYGVNITFSVETEPLGTAGPLKLAEDVLKK
   Consensus   (51) LAINYR PEVMLNFLKDFE KLGIKITCSQETEPLGTAGPLALARDKLID
                  101                                                 150
Arabidopsis1   (81) ESGQPFFVLNSDVICEYPLLEMIEFHKTNRAEASIMVTEVDDPSKYGVVV
Arabidopsis2  (100) GSGEPFFVLNSDVISEYPLKEMLEFHKSHGGEASIMVTKVDEPSKYGVVV
     Candida  (100) DN-SPFFVLNSDVICEYPFKELADFHKAHGGKGTIVATKVDEPSKYGVIV
       Maize  (100) GSGQPFFVLNSDVISEYPFAELIKFHKCHGGEATIMVTKVDEPSKYGVVV
       Oryza  (100) GSGEPFFVLNSDVISEYPFAELIKFHKSHGGEATIMVTKVDEPSKYGVVV
      Potato  (100) DSGEPFFVLNSDVISEYPFKEMIQFHKSHGGEASLMVTKVDEPSKYGVVV
     Tobacco  (100) DSGEPFFVLNSDVISEYPFKEMIAFHKSHGGEASLMVTKVDEPSKYGVVV
       Yeast  (100) DN-SPFFVLNSDVICEYPFKELADFHKAHGGKGTIVATKVDEPSKYGVIV
   Consensus  (101) DSGEPFFVLNSDVISEYPFKELIDFHKSHGGEASIMVTKVDEPSKYGVVV
                  151                                                 200
Arabidopsis1  (131) TEEGTA-RVESFVEKPKHFVGNKINAGIYLLSPSVLDRIELRRTSIEKEI
Arabidopsis2  (150) MEESTG-RVEKFVEKPKLYVGNKINAGIYLLNPSVLDKIELRPTSIEKET
     Candida  (149) HDIATPNLIDRFVEKPKEFVGNRINAGLYILNPEVIDLIEMKPTSIETET
       Maize  (150) MEEATG-RVERFVEKPKIFVGNKINAGIYLLNPSVLDRIELRPTSIEKEV
       Oryza  (150) MEEVTG-MVEKFVEKPKIFVGNKINAGIYLLNPSVLDRIELKPTSIEKEV
      Potato  (150) MEESTG-QVERFVEKPKLFVGNKINAGFYLLNPSVLDRIQLRPTSIEKEV
     Tobacco  (150) MEESTG-QVERFVEKPKLFVGNKINAGFYLLNPSVLDRIQLRPTSIEKEV
       Yeast  (149) HDIATPNLIDRFVEKPKEFVGNRINAGLYILNPEVIDLIEMKPTSIEKET
   Consensus  (151) MEEATG  VERFVEKPKLFVGNKINAGIYLLNPSVLDRIELRPTSIEKEV
                  201                                                 250
Arabidopsis1  (180) FPKIASEKKLYAMVLPGFWMDIGQPKDYITGQRMYLNSLREKTPQELATG
Arabidopsis2  (199) FPKIAAAQGLYAMVLPGFWMDIGQPRDYITGLRLYLDSLRKKSPAKLTSG
     Candida  (199) FPILVEQKSLYSFDLEGFWMDVGQPKDFLSGTVLYLNSVSKKNPEKLTKG
       Maize  (199) FPQIAADQQLYAMVLPGFWMDVGQPRDYITGLRLYLDSIRKKSAAKLATG
       Oryza  (199) FPRIASDAKLFALVLPGFWMDVGQPRDYITGLRLYLDSLRKRSTNRLATG
      Potato  (199) FPKIAAEKKLYAMVLPGFWMDIGQPRDYITGLRLYLDSLKKHSSPKLASG
     Tobacco  (199) FPKIAAEEKLYAMVLPGFWMDIGQPRDYIPGLRLYLDSLKKNSSPKLASG
       Yeast  (199) FPILVEEKQLYSFDLEGFWMDVGQPKDFLSGTVLYLNSLAKRQPKKLATG
   Consensus  (201) FPKIAAEKKLYAMVLPGFWMDIGQPRDYITGLRLYLDSLRKKSP KLATG
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